

Variation in susceptibility to HIV-1 infection depends on numerous factors, and host genetic variation has been well-described as an important component. As a transcriptional regulator, interferon regulatory factor 1 (IRF-1) plays a key role in both innate and adaptive immunity against viral infection. IRF-1 has also been shown to directly interact with HIV-1 5' LTR and efficiently initiate or amplify HIV-1 replication. By complete gene sequencing, we investigated genetic polymorphism of the IRF-1 gene in an HIV-1-endemic Kenyan population. This population displayed extensive genetic diversity at the IRF-1 locus. Fifty-three single nucleotide polymorphisms (SNPs) were identified in this population, including 26 novel SNPs. Two insertion and one deletion polymorphisms in IRF-1 were also identified. Linkage disequilibrium (LD) among these genetic variations was shown to be common in IRF-1. The functional consequences of these mutations in the context of HIV-1/AIDS remain to be determined. We also identified 35 consistent discrepancies between IRF-1 GenBank sequences and our population based sequencing data, suggesting that the previously submitted GenBank data were not representative of the majority of human IRF-1 sequences.